

Eugene Shakhnovich

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

3,443
citations

471371

17
h-index

434063

31
g-index

40
all docs

40
docs citations

40
times ranked

2517
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of antibacterial compounds that constrain evolutionary pathways to resistance. <i>ELife</i> , 2021, 10, .	2.8	12
2	Cotranslational folding allows misfolding-prone proteins to circumvent deep kinetic traps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1485-1495.	3.3	44
3	Validation of DBFOLD: An efficient algorithm for computing folding pathways of complex proteins. <i>PLoS Computational Biology</i> , 2020, 16, e1008323.	1.5	11
4	Stability of the Influenza Virus Hemagglutinin Protein Correlates with Evolutionary Dynamics. <i>MSphere</i> , 2018, 3, .	1.3	31
5	Exploring the Mutational Robustness of Nucleic Acids by Searching Genotype Neighborhoods in Sequence Space. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 407-414.	2.1	11
6	Rational Design of Novel Allosteric Dihydrofolate Reductase Inhibitors Showing Antibacterial Effects on Drug-Resistant <i>Escherichia coli</i> Escape Variants. <i>ACS Chemical Biology</i> , 2017, 12, 1848-1857.	1.6	22
7	Benchmarking Inverse Statistical Approaches for Protein Structure and Design with Exactly Solvable Models. <i>PLoS Computational Biology</i> , 2016, 12, e1004889.	1.5	43
8	Searching the Sequence Space for Potent Aptamers Using SELEX in Silico. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 5939-5946.	2.3	27
9	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	3.1	188
10	Soluble oligomerization provides a beneficial fitness effect on destabilizing mutations.. <i>Nature Precedings</i> , 2011, , .	0.1	0
11	Topology of protein interaction network shapes protein abundances and strengths of their functional and nonspecific interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4258-4263.	3.3	94
12	Protein folding roller coaster, one molecule at a time. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11823-11824.	3.3	4
13	Protein Folding Thermodynamics and Dynamics: Where Physics, Chemistry, and Biology Meet. <i>Chemical Reviews</i> , 2006, 106, 1559-1588.	23.0	332
14	On the origin and highly likely completeness of single-domain protein structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2605-2610.	3.3	182
15	Protein structure and evolutionary history determine sequence space topology. <i>Genome Research</i> , 2005, 15, 385-392.	2.4	82
16	Phase Transformations and Orientational Ordering in Chemically Disordered Polymers – a Modern Primer. , 2004, , 455-484.		0
17	Field theory and segmental alignment analysis for a solution of sequence disordered liquid crystalline polymers. <i>Journal of Chemical Physics</i> , 2002, 116, 3134-3140.	1.2	1
18	Exotic phase transitions in disordered globular networks. <i>Journal of Chemical Physics</i> , 2001, 114, 10968-10976.	1.2	2

#	ARTICLE	IF	CITATIONS
19	Protein Folding Theory: From Lattice to All-Atom Models. Annual Review of Biophysics and Biomolecular Structure, 2001, 30, 361-396.	18.3	326
20	Evolutionary conservation of the folding nucleus ¹ Edited by A. R. Fersht. Journal of Molecular Biology, 2001, 308, 123-129.	2.0	116
21	Orientalional ordering in sequence-disordered liquid crystalline polymers. Chemical Physics Letters, 2000, 325, 323-329.	1.2	4
22	Freezing in polyampholytes globules: Influence of the long-range nature of the interaction. Journal of Chemical Physics, 1999, 111, 772-785.	1.2	8
23	On the role of conformational geometry in protein folding. Journal of Chemical Physics, 1999, 111, 10375-10380.	1.2	28
24	Disordered heteropolymers with cross-links α phase diagram and conformational transitions. Chemical Physics Letters, 1999, 303, 355-362.	1.2	4
25	Factors that affect the folding ability of proteins. , 1999, 35, 34-40.		45
26	A strategy for detecting the conservation of folding-nucleus residues in protein superfamilies. Folding & Design, 1998, 3, 239-251.	4.5	49
27	Phase diagram analysis of random heteropolymers with composition specific and quenched cross-links. Journal of Chemical Physics, 1998, 109, 2947-2958.	1.2	7
28	Frozen phases with re-entrant transition for random heteropolymers with composition specific and annealed cross-links. Journal of Chemical Physics, 1997, 107, 1247-1258.	1.2	7
29	Protein Dynamics. , 1996, , 113-126.		0
30	Protein dynamics: From the native to the unfolded state and back again. Molecular Engineering, 1995, 5, 55-70.	0.2	1
31	Protein Dynamics: From the Native to the Unfolded State and Back Again. Jerusalem Symposia on Quantum Chemistry and Biochemistry, 1995, , 69-84.	0.2	5
32	How does a protein fold?. Nature, 1994, 369, 248-251.	13.7	934
33	Statistical mechanics of proteins with α -evolutionary selected β sequences. Physical Review E, 1994, 50, 1303-1312.	0.8	69
34	Kinetics of Protein Folding. Journal of Molecular Biology, 1994, 235, 1614-1636.	2.0	513
35	Enumeration of all compact conformations of copolymers with random sequence of links. Journal of Chemical Physics, 1990, 93, 5967-5971.	1.2	240